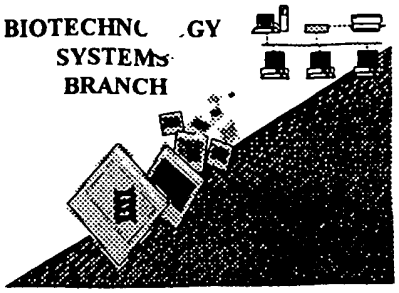
0300 0400 02-14-0

BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/756,398

Source: OIPE

Date Processed by STIC: 01/25/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW.

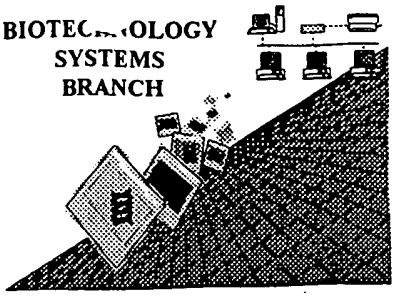
Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). **Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.**

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

6420

BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

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Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). [illegible] to filing the sequence listing is expected to result in fewer errored sequence [illegible] saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/756,398

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 ____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 ____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 ____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

8 ____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 ____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 ____ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 ____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

#2

OIPE

RAW SEQUENCE LISTING DATE: 01/25/2001
PATENT APPLICATION: US/09/756,398 TIME: 11:15:31

Input Set : A:\0975.1005-006SEQLIST.TXT
Output Set: N:\CRF3\01252001\I756398.raw

Does Not Comply
Corrected Diskette Needed

pgs 1-5

```
 4 <110> APPLICANT: Junming Le
 5       Jan Vilcek
 6       Peter Daddona
 7       John Ghrayeb
 8       David M. Knight
 9       Scott Siegel
11 <120> TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
12       Human Tumor Necrosis Factor
15 <130> FILE REFERENCE: 0975.1005-006
17 <140> CURRENT APPLICATION NUMBER: US/09/756,398
17 <141> CURRENT FILING DATE: 2001-01-08
17 <150> PRIOR APPLICATION NUMBER: U.S. 09/133,119
18 <151> PRIOR FILING DATE: 1998-08-12
20 <150> PRIOR APPLICATION NUMBER: U.S. 08/570,674
21 <151> PRIOR FILING DATE: 1995-12-11
23 <150> PRIOR APPLICATION NUMBER: U.S. 08/324,799
24 <151> PRIOR FILING DATE: 1994-10-18
26 <150> PRIOR APPLICATION NUMBER: U.S. 08/192,102
27 <151> PRIOR FILING DATE: 1994-02-04
29 <150> PRIOR APPLICATION NUMBER: U.S. 08/192,861
30 <151> PRIOR FILING DATE: 1994-02-04
32 <150> PRIOR APPLICATION NUMBER: U.S. 08/192,093
33 <151> PRIOR FILING DATE: 1994-02-04
35 <150> PRIOR APPLICATION NUMBER: U.S. 08/010,406
36 <151> PRIOR FILING DATE: 1993-01-29
38 <150> PRIOR APPLICATION NUMBER: U.S. 08/013,413
39 <151> PRIOR FILING DATE: 1993-02-02
41 <150> PRIOR APPLICATION NUMBER: U.S. 07/943,852
42 <151> PRIOR FILING DATE: 1992-09-11
44 <150> PRIOR APPLICATION NUMBER: U.S. 07/853,606
45 <151> PRIOR FILING DATE: 1992-03-18
47 <150> PRIOR APPLICATION NUMBER: U.S. 07/670,827
48 <151> PRIOR FILING DATE: 1991-03-18
50 <160> NUMBER OF SEQ ID NOS: 19
52 <170> SOFTWARE: FastSEQ for Windows Version 4.0
54 <210> SEQ ID NO: 1
55 <211> LENGTH: 157
56 <212> TYPE: PRT
57 <213> ORGANISM: Peptide
59 <400> SEQUENCE: 1
60 Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
61  1               5                  10                  15
62 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
63             20                  25                  30
64 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
65         35                  40                  45
66 Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
```

GLOBAL ERROR

invalid response - per 1.823 of new Sequence Rules, the only valid <213> response are: Unknown, Artificial Sequence, or scientific name (genus/species) (one of the three) (see circled portion of item 12 on Error Summary Sheet)

RAW SEQUENCE LISTING DATE: 01/25/2001
PATENT APPLICATION: US/09/756,398 TIME: 11:15:31

Input Set : A:\0975.1005-006SEQLIST.TXT
Output Set: N:\CRF3\01252001\I756398.raw

```
     50                  55                  60
Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
65                  70                  75                  80
Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
                85                  90                  95
Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
            100                 105                 110
Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
        115                 120                 125
Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
    130                 135                 140
Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145                 150                 155
<210> SEQ ID NO: 2
<211> LENGTH: 321
<212> TYPE: DNA
<213> ORGANISM: cDNA
<220> FEATURE:
<221> NAME/KEY: CDS
W--> <222> LOCATION: (0)...(321)
<400> SEQUENCE: 2
gac atc ttg ctg act cag tct cca gcc atc ctg tct gtg agt cca gga   48
Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
 1               5                  10                  15
gaa aga gtc agt ttc tcc tgc agg gcc agt cag ttc gtt ggc tca agc   96
Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
            20                  25                  30
atc cac tgg tat cag caa aga aca aat ggt tct cca agg ctt ctc ata   144
Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
        35                  40                  45
aag tat gct tct gag tct atg tct ggg atc cct tcc agg ttt agt ggc   192
Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60
agt gga tca ggg aca gat ttt act ctt agc atc aac act gtg gag tct   240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
65                  70                  75                  80
gaa gat att gca gat tat tac tgt caa caa agt cat agc tgg cca ttc   288
Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
                85                  90                  95
acg ttc ggc tcg ggg aca aat ttg gaa gta aaa                       321
Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
            100                 105
<210> SEQ ID NO: 3
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Protein
<400> SEQUENCE: 3
Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
 1               5                  10                  15
```

see previous page regarding valid <2137 response
(1) → first base begins at location 1

RAW SEQUENCE LISTING DATE: 01/25/2001
PATENT APPLICATION: US/09/756,398 TIME: 11:15:31

Input Set : A:\0975.1005-006SEQLIST.TXT
Output Set: N:\CRF3\01252001\I756398.raw

```
129 Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
130             20                  25                  30
131 Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
132         35                  40                  45
133 Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
134     50                  55                  60
135 Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
136 65                  70                  75                  80
137 Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
138                 85                  90                  95
139 Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
140             100                 105
143 <210> SEQ ID NO: 4
144 <211> LENGTH: 357
145 <212> TYPE: DNA
146 <213> ORGANISM: cDNA
148 <220> FEATURE:
149 <221> NAME/KEY: CDS
W--> 150 <222> LOCATION: (0)...(357)
152 <400> SEQUENCE: 4
153 gaa gtg aag ctt gag gag tct gga gga ggc ttg gtg caa cct gga gga   48
154 Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
155  1               5                  10                  15
157 tcc atg aaa ctc tcc tgt gtt gcc tct gga ttc att ttc agt aac cac   96
158 Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
159              20                  25                  30
161 tgg atg aac tgg gtc cgc cag tct cca gag aag ggg ctt gag tgg gtt   144
162 Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
163          35                  40                  45
165 gct gaa att aga tca aaa tct att aat tct gca aca cat tat gcg gag   192
166 Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
167      50                  55                  60
169 tct gtg aaa ggg agg ttc acc atc tca aga gat gat tcc aaa agt gct   240
170 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala
171  65                  70                  75                  80
173 gtc tac ctg caa atg acc gac tta aga act gaa gac act ggc gtt tat   288
174 Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr
175                  85                  90                  95
177 tac tgt tcc agg aat tac tac ggt agt acc tac gac tac tgg ggc caa   336
178 Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
179              100                 105                 110
181 ggc acc act ctc aca gtc tcc                                     357
182 Gly Thr Thr Leu Thr Val Ser
183          115
186 <210> SEQ ID NO: 5
187 <211> LENGTH: 119
188 <212> TYPE: PRT
189 <213> ORGANISM: Protein
191 <400> SEQUENCE: 5
```

RAW SEQUENCE LISTING DATE: 01/25/2001
PATENT APPLICATION: US/09/756,398 TIME: 11:15:31

Input Set : A:\0975.1005-006SEQLIST.TXT
Output Set: N:\CRF3\01252001\I756398.raw

```
192 Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
193  1               5                  10                  15
194 Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
195             20                  25                  30
196 Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
197         35                  40                  45
198 Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
199     50                  55                  60
200 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala
201 65                  70                  75                  80
202 Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr
203                 85                  90                  95
204 Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
205             100                 105                 110
206 Gly Thr Thr Leu Thr Val Ser
207         115
```

210 <210> SEQ ID NO: 6
211 <211> LENGTH: 8
212 <212> TYPE: PRT
213 <213> ORGANISM: Protein
215 <400> SEQUENCE: 6

```
216 Gly Thr Leu Val Thr Val Ser Ser
217  1               5
```

220 <210> SEQ ID NO: 7
221 <211> LENGTH: 7
222 <212> TYPE: PRT
223 <213> ORGANISM: Protein
225 <400> SEQUENCE: 7

```
226 Gly Thr Lys Leu Glu Ile Lys
227  1               5
```

230 <210> SEQ ID NO: 8
231 <211> LENGTH: 20
232 <212> TYPE: DNA
233 <213> ORGANISM: cDNA
235 <400> SEQUENCE: 8

236 cctggatacc tgtgaaaaga 20

238 <210> SEQ ID NO: 9
239 <211> LENGTH: 27
240 <212> TYPE: DNA
241 <213> ORGANISM: cDNA
243 <400> SEQUENCE: 9

244 cctggtacct tagtcaccgt ctcctca 27

246 <210> SEQ ID NO: 10
247 <211> LENGTH: 27
248 <212> TYPE: DNA
249 <213> ORGANISM: cDNA
251 <400> SEQUENCE: 10

252 aatagatatc tccttcaaca cctgcaa 27

254 <210> SEQ ID NO: 11

RAW SEQUENCE LISTING DATE: 01/25/2001
PATENT APPLICATION: US/09/756,398 TIME: 11:15:31

Input Set : A:\0975.1005-006SEQLIST.TXT
Output Set: N:\CRF3\01252001\I756398.raw

255 <211> LENGTH: 21
256 <212> TYPE: DNA
257 <213> ORGANISM: cDNA
259 <400> SEQUENCE: 11
260 atcgggacaa agttggaaat a 21
262 <210> SEQ ID NO: 12
263 <211> LENGTH: 16
264 <212> TYPE: DNA
265 <213> ORGANISM: cDNA
267 <400> SEQUENCE: 12
268 ggcggtctgg taccgg 16
270 <210> SEQ ID NO: 13
271 <211> LENGTH: 19
272 <212> TYPE: DNA
273 <213> ORGANISM: cDNA
275 <400> SEQUENCE: 13
276 gtcaacaaca tagtcatca 19
278 <210> SEQ ID NO: 14
279 <211> LENGTH: 23
280 <212> TYPE: DNA
281 <213> ORGANISM: cDNA
283 <400> SEQUENCE: 14
284 cacaggtgtg tccccaagga aaa 23
286 <210> SEQ ID NO: 15
287 <211> LENGTH: 18
288 <212> TYPE: DNA
289 <213> ORGANISM: cDNA
291 <400> SEQUENCE: 15
292 aatctggggt aggcacaa 18
294 <210> SEQ ID NO: 16
295 <211> LENGTH: 17
296 <212> TYPE: DNA
297 <213> ORGANISM: cDNA
299 <400> SEQUENCE: 16
300 agtgtgtgtc cccaagg 17
302 <210> SEQ ID NO: 17
303 <211> LENGTH: 24
304 <212> TYPE: DNA
305 <213> ORGANISM: cDNA
307 <400> SEQUENCE: 17
308 cacagctgcc cgcccaggtg gcat 24
310 <210> SEQ ID NO: 18
311 <211> LENGTH: 17
312 <212> TYPE: DNA
313 <213> ORGANISM: cDNA
315 <400> SEQUENCE: 18
316 gtcgccagtg ctccctt 17
318 <210> SEQ ID NO: 19 → Please ensure <213> response is valid
319 <211> LENGTH: 20

VERIFICATION SUMMARY DATE: 01/25/2001
PATENT APPLICATION: US/09/756,398 TIME: 11:15:32

Input Set : A:\0975.1005-006SEQLIST.TXT
Output Set: N:\CRF3\01252001\I756398.raw

L:17 M:270 C: Current Application Number differs, Replaced Current Application No
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:89 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:2, CDS LOCATION: (321)
L:150 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:4, CDS LOCATION: (0)...(357)